

CLAIMS

What is claimed is:

1 1. A method for estimating the precision of measurements taken from an
2 array, comprising:

- 3 (a) identifying a set of low-level data measurements;
4 (b) estimating a standard deviation, σ_e , of an additive error component, ϵ ;
5 (c) estimating a background parameter, α ;
6 (d) identifying a set of replicated high-level data measurements;
7 (e) estimating a standard deviation, σ_n , from the standard deviation of
8 the logarithm of the replicated high-level data set;
9 (f) measuring a signal, y , wherein said signal indicates an amount of a
10 biological molecule; and
11 (g) estimating a variance of the measured signal as

12
$$\text{Var}(\hat{\mu}) = \hat{\sigma}_e^2 + \hat{\mu}^2 e^{\hat{\sigma}_n^2} (e^{\hat{\sigma}_n^2} - 1), \text{ where } \hat{\mu}^2 = (y - \alpha)^2.$$

1 2. The method of claim 1, wherein said identifying step (a) comprises the
2 use of a thresholding algorithm to establish a cutoff, and the set of low-level data
3 consists of those data with values less than the cutoff.

1 3. The method of claim 2, wherein the thresholding algorithm comprises
2 the steps of:

- 3 (a) identifying A_N , an initial set of low-level data measurements consisting
4 of q percent of the total number of data points having the lowest
5 measurement values, $A_N = \{x_1, x_2, \dots, x_{no}\}$;
6 (b) calculating a mean and a standard deviation of the initial set;
7 (c) calculating a cutoff point, $u_N = \text{mean} + c \times \text{the standard deviation}$,
8 wherein $2 \leq c \leq 3$;
9 (d) defining a new set, $A_{N+1} = \{x_j < u_N\}$;
10 (e) calculating a mean and standard deviation of the new set; and
11 (f) repeating steps (c) and (d) using the mean and standard deviation of the
12 new set until the algorithm converges.

1 4. The method of claim 2, wherein the thresholding algorithm comprises
2 the steps of:

- 3 (a) identifying A_N , an initial set, of low-level data consisting of q percent
4 of the total number of data points having the lowest measurement
5 values, $A_N = \{x_1, x_2, \dots, x_{no}\}$;
- 6 (b) calculating a median of the initial set, $m_0 = \text{median} \{x_j\}_{j=1}^{n_0}$ and a
7 median of the absolute deviations about the median,
8 $MAD_0 = \text{median} \{|x_j - m_0|\}_{j=1}^{n_0}$;
- 9 (c) calculating a cutoff point, $u_0 = MAD_0 + c \times s_0$, wherein $s_0 =$
10 $MAD_0/0.675$ and $2 \leq c \leq 3$;
- 11 (d) defining a new set, $A_{N+1} = \{x_j < u_N\}$;
- 12 (e) calculating a median and a median of the absolute deviations about the
13 median of the new set; and
- 14 (f) repeating steps (c) and (d) using the median and the median of the
15 absolute deviations about the median of the new set until the algorithm
16 converges.

1 5. The method of claim 2, wherein the mean of the low-level data
2 measurements is used as the estimate of the background parameter, α .

1 6. The method of claim 1, wherein the standard deviation of the low-level
2 data measurements is used as the estimate of the parameter σ_e .

1 7. The method of claim 1, wherein, a mean of negative control data is
2 used as the estimate of the background parameter, α .

1 8. The method of claim 1, wherein the biological molecule is a nucleic
2 acid.

1 9. The method of claim 8, wherein the nucleic acid is mRNA.

1 10. The method of claim 8, wherein the biological molecule is DNA.

1 11. The method of claim 10, wherein the DNA is cDNA.

1 12. The method of claim 10, wherein the DNA is genomic.

1 13. The method of claim 1, wherein the biological molecule is a protein.

1 14. The method of claim 1, wherein the biological molecule is a lipid.